Figure 1A

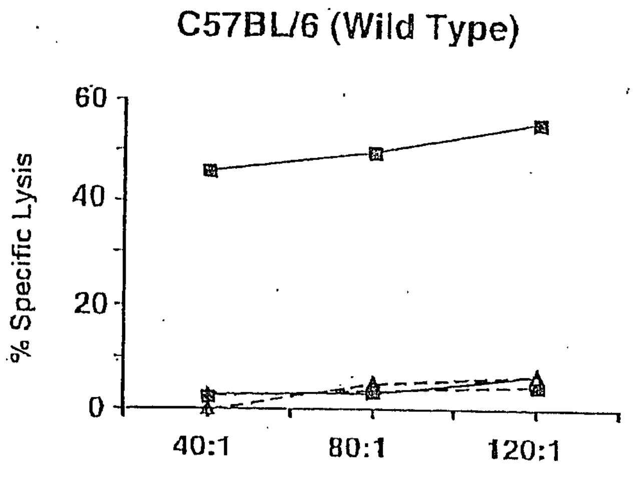
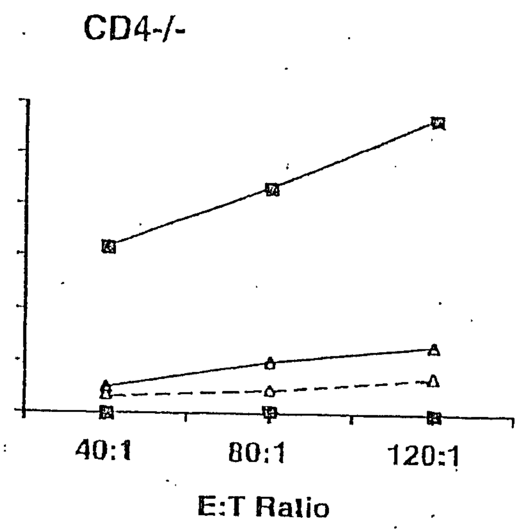


Figure 1B



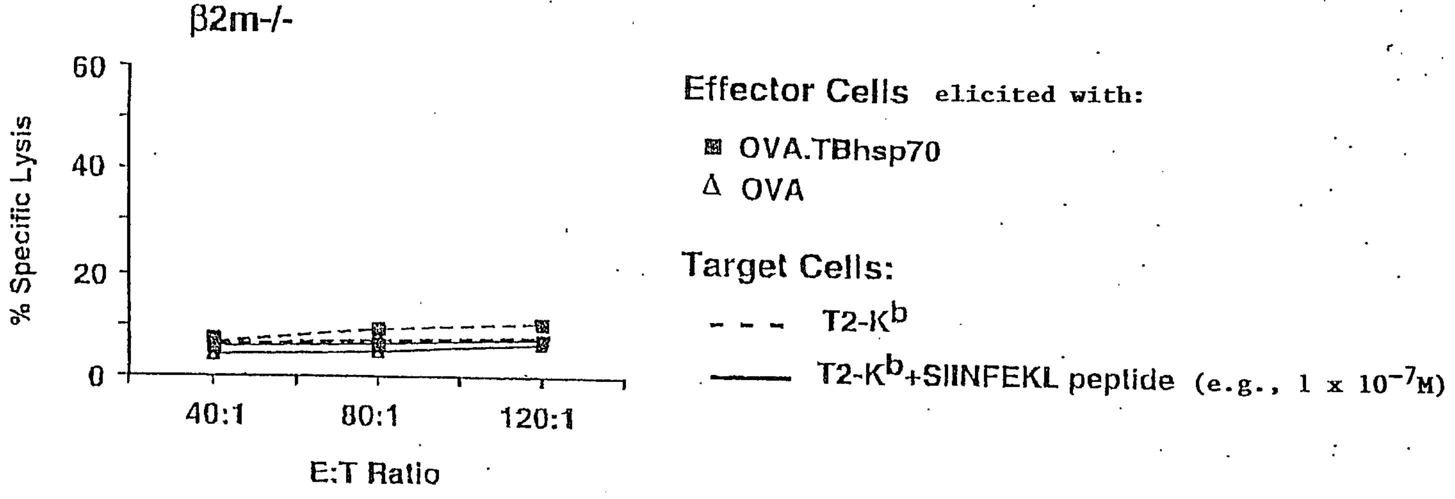


Figure 1C

Figure 2A

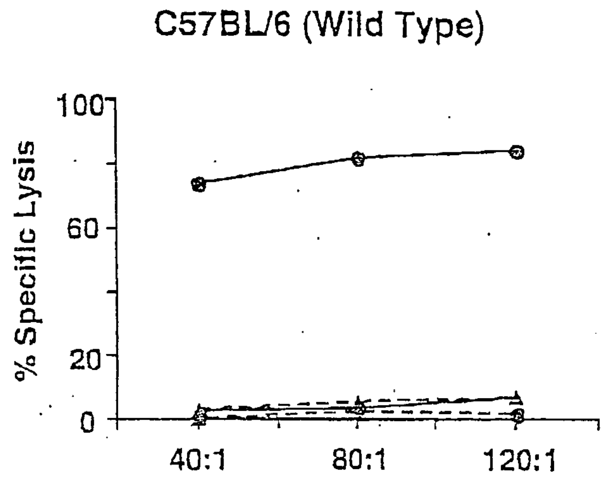
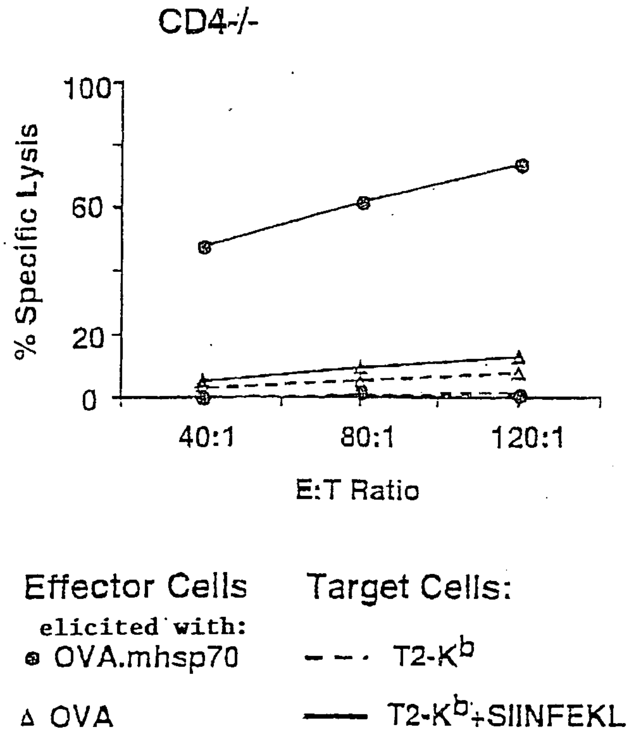


Figure 2B



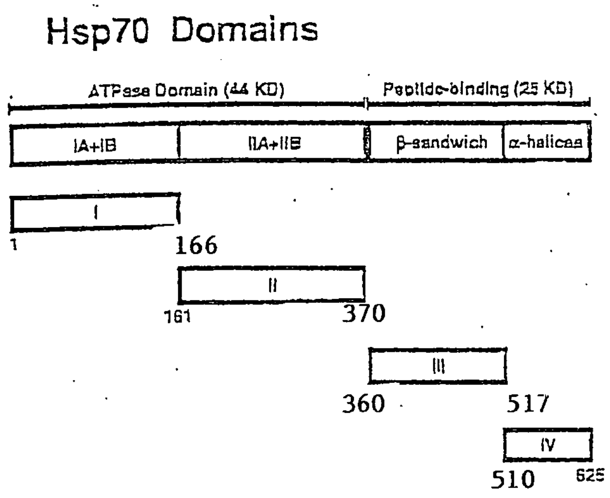

Hsp70 Domains
ATPase Domain (44 KD)
Peptide-binding (25 KD)
IA+IB
IIA+IIB
β-sandwich
α-helices
I
1
166
II
161
370
III
360
517
IV
510
625

Figure 3

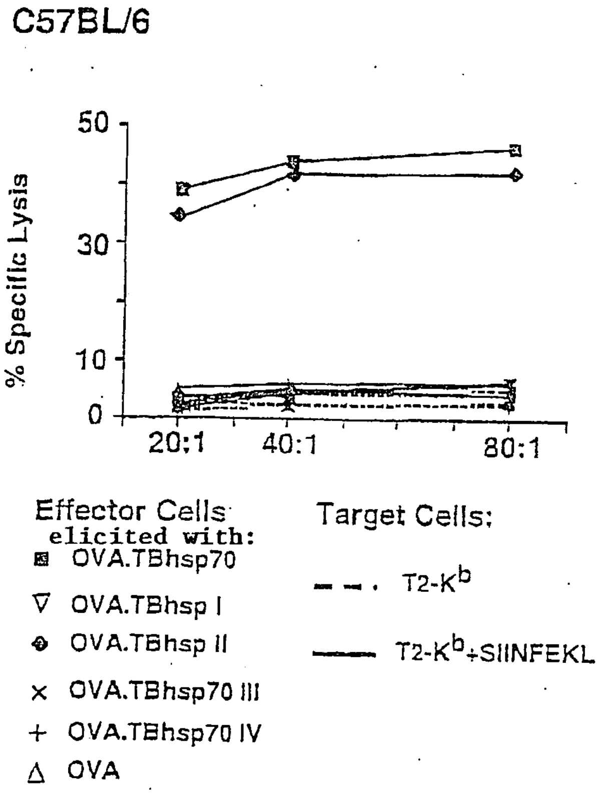

C57BL/6
% Specific Lysis
50
30
10
0
20:1
40:1
80:1
Effector Cells elicited with:
▣ OVA.TBhsp70
∇ OVA.TBhsp I
◈ OVA.TBhsp II
× OVA.TBhsp70 III
+ OVA.TBhsp70 IV
Δ OVA
Target Cells:
- - . T2-K^b
—— T2-K^b+SIINFEKL

Figure 4

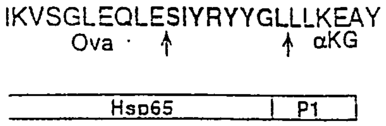


Figure 5A

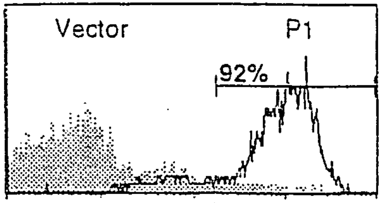


Figure 5B

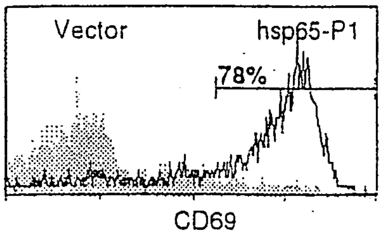


Figure 5C

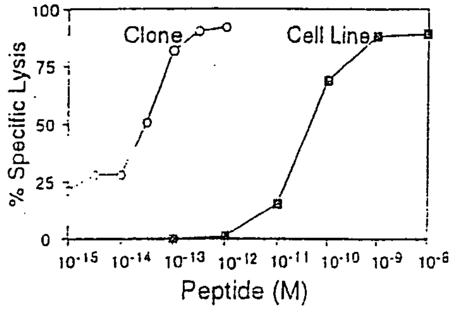


Figure 5D

Figure 6A

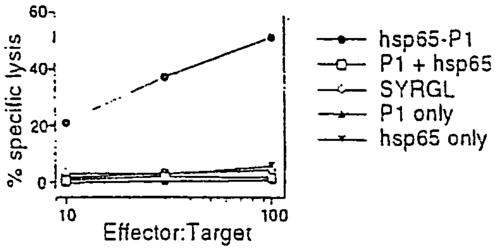


Figure 6B

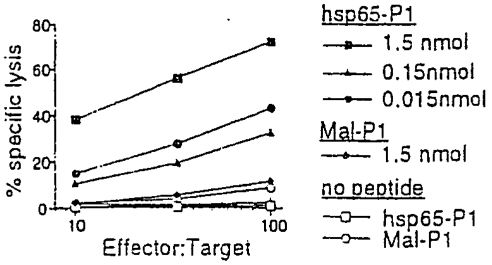
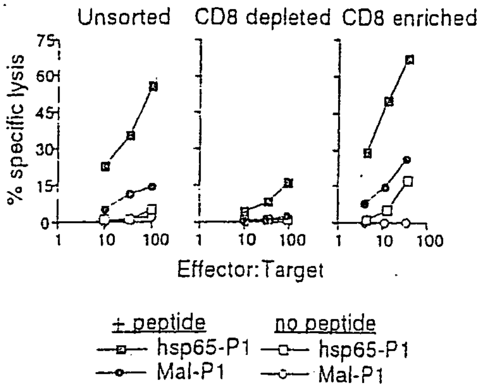


Figure 6C



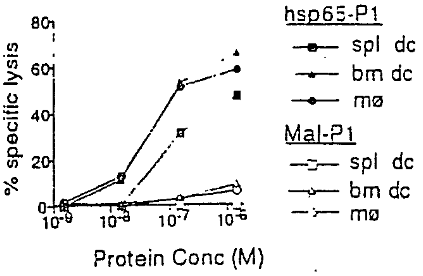

80
60
40
20
0
% specific lysis
10-9
10-8
10-7
10-6
Protein Conc (M)
hsp65-P1
spl dc
bm dc
mø
Mal-P1
spl dc
bm dc
mø

Figure 7

Figure 8A

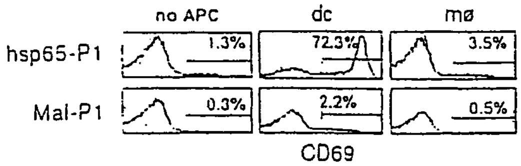


Figure 8B

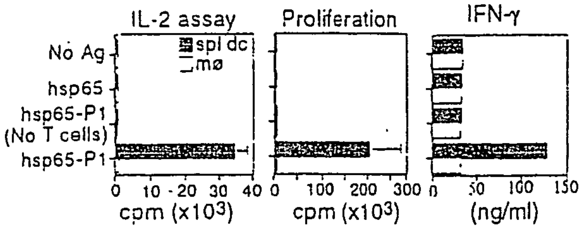


Figure 8C

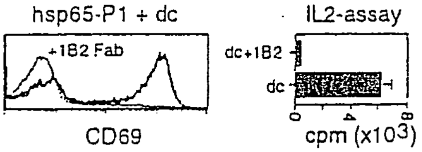


Figure 9A

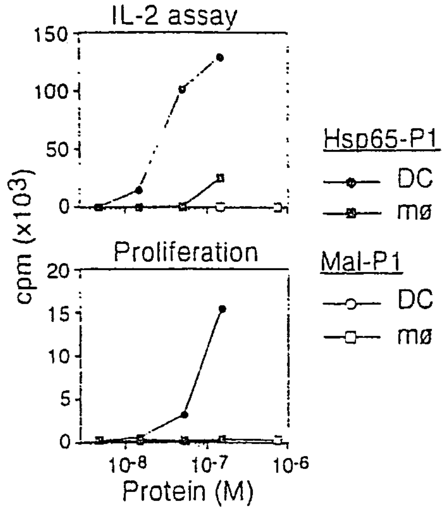


Figure 9B

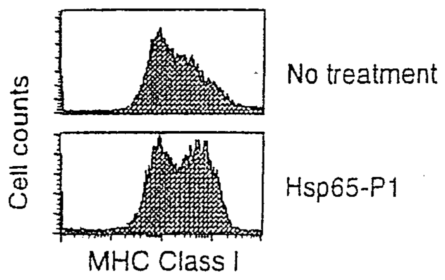
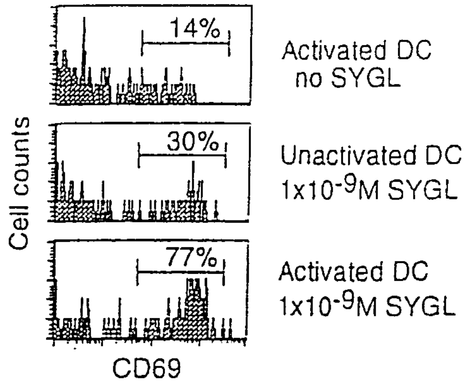


Figure 9C



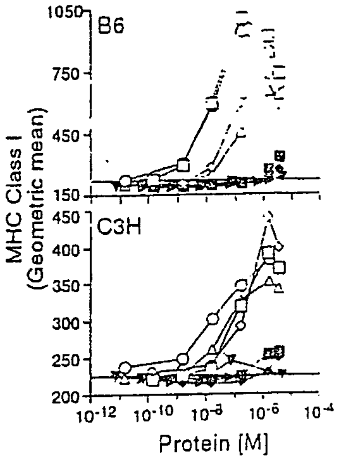


Figure 10A

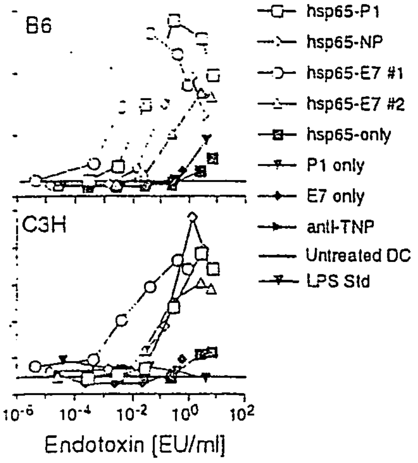


Figure 10B

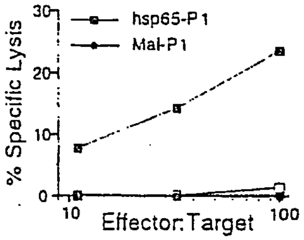


Figure 10C

```
TBhsp70 (cDNA) -> Translate • 1-frame

DNA sequence    1879 bp    ATGGCTCGTGCG ... AGGCCAAGTGAC    linear


1/1                                     31/11
ATG GCT CGT GCG GTC GGG ATC GAC CTC GGG ACC ACC AAC TCC GTC GTC TCG GTT CTG GAA
M   A   R   A   V   G   I   D   L   G   T   T   N   S   V   V   S   V   L   E
61/21                                   91/31
GGT GGC GAC CCG GTC GTC GTC GCC AAC TCC GAG GGC TCC AGG ACC ACC CCG TCA ATT GTC
G   G   D   P   V   V   V   A   N   S   E   G   S   R   T   T   P   S   I   V
121/41                                  151/51
GCG TTC GCC CGC AAC GGT GAG GTG CTG GTC GGC CAG CCC GCC AAG AAC CAG GCA GTG ACC
A   F   A   R   N   G   E   V   L   V   G   Q   P   A   K   N   Q   A   V   T
181/61                                  211/71
AAC GTC GAT CGC ACC GTG CGC TCG GTC AAG CGA CAC ATG GGC AGC GAC TGG TCC ATA GAG
N   V   D   R   T   V   R   S   V   K   R   H   M   G   S   D   W   S   I   E
241/81                                  271/91
ATT GAC GGC AAG AAA TAC ACC GCG CCG GAG ATC AGC GCC CGC ATT CTG ATG AAG CTG AAG
I   D   G   K   K   Y   T   A   P   E   I   S   A   R   I   L   M   K   L   K
301/101                                 331/111
CGC GAC GCC GAG GCC TAC CTC GGT GAG GAC ATT ACC GAC GCG GTT ATC ACG ACG CCC GCC
R   D   A   E   A   Y   L   G   E   D   I   T   D   A   V   I   T   T   P   A
361/121                                 391/131
TAC TTC AAT GAC GCC CAG CGT CAG GCC ACC AAG GAC GCC GGC CAG ATC GCC GGC CTC AAC
Y   F   N   D   A   Q   R   Q   A   T   K   D   A   G   Q   I   A   G   L   N
421/141                                 451/151
GTG CTG CGG ATC GTC AAC GAG CCG ACC GCG GCC GCG CTG GCC TAC GGC CTC GAC AAG GGC
V   L   R   I   V   N   E   P   T   A   A   A   L   A   Y   G   L   D   K   G
481/161                                 511/171
GAG AAG GAG CAG CGA ATC CTG GTC TTC GAC TTG GGT GGT GGC ACT TTC GAC GTT TCC CTG
E   K   E   Q   R   I   L   V   F   D   L   G   G   G   T   F   D   V   S   L
541/181                                 571/191
CTG GAG ATC GGC GAG GGT GTG GTT GAG GTC CGT GCC ACT TCG GGT GAC AAC CAC CTC GGC
L   E   I   G   E   G   V   V   E   V   R   A   T   S   G   D   N   H   L   G
601/201                                 631/211
GGC GAC GAC TGG GAC CAG CGG GTC GTC GAT TGG CTG GTG GAC AAG TTC AAG GGC ACC AGC
G   D   D   W   D   Q   R   V   V   D   W   L   V   D   K   F   K   G   T   S
661/221                                 691/231
GGC ATC GAT CTG ACC AAG GAC AAG ATG GCG ATG CAG CGG CTG CGG GAA GCC GCC GAG AAG
G   I   D   L   T   K   D   K   M   A   M   Q   R   L   R   E   A   A   E   K
721/241                                 751/251
GCA AAG ATC GAG CTG AGT TCG AGT CAG TCC ACC TCG ATC AAC CTG CCC TAC ATC ACC GTC
A   K   I   E   L   S   S   S   Q   S   T   S   I   N   L   P   Y   I   T   V
781/261                                 811/271
GAC GCC GAC AAG AAC CCG TTG TTC TTA GAC GAG CAG CTG ACC CGC GCG GAG TTC CAA CGG
D   A   D   K   N   P   L   F   L   D   E   Q   L   T   R   A   E   F   Q   R
841/281                                 871/291
ATC ACT CAG GAC CTG CTG GAC CGC ACT CGC AAG CCG TTC CAG TCG GTG ATC GCT GAC ACC
I   T   Q   D   L   L   D   R   T   R   K   P   F   Q   S   V   I   A   D   T
901/301                                 931/311
GGC ATT TCG GTG TCG GAG ATC GAT CAC GTT GTG CTC GTG GGT GGT TCG ACC CGG ATG CCC
G   I   S   V   S   E   I   D   H   V   V   L   V   G   G   S   T   R   M   P
961/321                                 991/331
GCG GTG ACC GAT CTG GTC AAG GAA CTC ACC GGC GGC AAG GAA CCC AAC AAG GGC GTC AAC
A   V   T   D   L   V   K   E   L   T   G   G   K   E   P   N   K   G   V   N
1021/341                                1051/351
CCC GAT GAG GTT GTC GCG GTG GGA GCC GCT CTG CAG GCC GGC GTC CTC AAG GGC GAG GTG
P   D   E   V   V   A   V   G   A   A   L   Q   A   G   V   L   K   G   E   V
1081/361                                1111/371
AAA GAC GTT CTG CTG CTT GAT GTT ACC CCG CTG AGC CTG GGT ATC GAG ACC AAG GGC GGG
K   D   V   L   L   L   D   V   T   P   L   S   L   G   I   E   T   K   G   G
1141/381                                1171/391
GTG ATG ACC AGG CTC ATC GAG CGC AAC ACC ACG ATC CCC ACC AAG CGG TCG GAG ACT TTC
V   M   T   R   L   I   E   R   N   T   T   I   P   T   K   R   S   E   T   F
1201/401                                1231/411
ACC ACC GCC GAC GAC AAC CAA CCG TCG GTG CAG ATC CAG GTC TAT CAG GGG GAG CGT GAG
T   T   A   D   D   N   Q   P   S   V   Q   I   Q   V   Y   Q   G   E   R   E
```

Figure 11

```
TBhsp70 (cDNA) -> Translate • 1-frame

DNA sequence       1879 bp   ATGGCTCGTGCG ... AGGCCAAGTGAC   linear
```

```
481/161                                           511/171
GAG AAG GAG CAG CGA ATC CTG GTC TTC GAC TTG GGT GGT GGC ACT TTC GAC GTT TCC CTG
E   K   E   Q   R   I   L   V   F   D   L   G   G   G   T   F   D   V   S   L
541/181                                           571/191
CTG GAG ATC GGC GAG GGT GTG GTT GAG GTC CGT GCC ACT TCG GGT GAC AAC CAC CTC GGC
L   E   I   G   E   G   V   V   E   V   R   A   T   S   G   D   N   H   L   G
601/201                                           631/211
GGC GAC GAC TGG GAC CAG CGG GTC GTC GAT TGG CTG GTG GAC AAG TTC AAG GGC ACC AGC
G   D   D   W   D   Q   R   V   V   D   W   L   V   D   K   F   K   G   T   S
661/221                                           691/231
GGC ATC GAT CTG ACC AAG GAC AAG ATG GCG ATG CAG CGG CTG CGG GAA GCC GCC GAG AAG
G   I   D   L   T   K   D   K   M   A   M   Q   R   L   R   E   A   A   E   K
721/241                                           751/251
GCA AAG ATC GAG CTG AGT TCG AGT CAG TCC ACC TCG ATC AAC CTG CCC TAC ATC ACC GTC
A   K   I   E   L   S   S   S   Q   S   T   S   I   N   L   P   Y   I   T   V
781/261                                           811/271
GAC GCC GAC AAG AAC CCG TTG TTC TTA GAC GAG CAG CTG ACC CGC GCG GAG TTC CAA CGG
D   A   D   K   N   P   L   F   L   D   E   Q   L   T   R   A   E   F   Q   R
841/281                                           871/291
ATC ACT CAG GAC CTG CTG GAC CGC ACT CGC AAG CCG TTC CAG TCG GTG ATC GCT GAC ACC
I   T   Q   D   L   L   D   R   T   R   K   P   F   Q   S   V   I   A   D   T
901/301                                           931/311
GGC ATT TCG GTG TCG GAG ATC GAT CAC GTT GTG CTC GTG GGT GGT TCG ACC CGG ATG CCC
G   I   S   V   S   E   I   D   H   V   V   L   V   G   G   S   T   R   M   P
961/321                                           991/331
GCG GTG ACC GAT CTG GTC AAG GAA CTC ACC GGC GGC AAG GAA CCC AAC AAG GGC GTC AAC
A   V   T   D   L   V   K   E   L   T   G   G   K   E   P   N   K   G   V   N
1021/341                                          1051/351
CCC GAT GAG GTT GTC GCG GTG GGA GCC GCT CTG CAG GCC GGC GTC CTC AAG GGC GAG GTG
P   D   E   V   V   A   V   G   A   A   L   Q   A   G   V   L   K   G   E   V
1081/361                                          1111/371
AAA GAC GTT CTG CTG CTT GAT GTT ACC CCG
K   D   V   L   L   L   D   V   T   P
```

Figure 12

```
murine hsp70.1 -> Translate • 1-frame

DNA  sequence       1929  bp   ATGGCCAAGAAC ... GAGGTGGATTAG   linear


                                                 31/11
1/1
ATG GCC AAG AAC ACG GCG ATC GGC ATC GAC CTG GGC ACC ACC TAC TCG TGC GTG GGC GTG
M   A   K   N   T   A   I   G   I   D   L   G   T   T   Y   S   C   V   G   V
61/21                                            91/31
TTC CAG CAC GGC AAG GTG GAG ATC ATC GCC AAC GAC CAG GGC AAC CGC ACG ACC CCC AGC
F   Q   H   G   K   V   E   I   I   A   N   D   Q   G   N   R   T   T   P   S
121/41                                           151/51
TAC GTG GCC TTC ACC GAC ACC GAG CGC CTC ATC GGG GAC GCC GCC AAG AAC CAG GTG GCG
Y   V   A   F   T   D   T   E   R   L   I   G   D   A   A   K   N   Q   V   A
181/61                                           211/71
CTG AAC CCG CAG AAC ACC GTG TTC GAC GCG AAG CGG CTG ATC GGC CGC AAG TTC GGC GAT
L   N   P   Q   N   T   V   F   D   A   K   R   L   I   G   R   K   F   G   D
241/81                                           271/91
GCG GTG GTG CAG TCC GAC ATG AAG CAC TGG CCC TTC CAG GTG GTG AAC GAC GGC GAC AAG
A   V   V   Q   S   D   M   K   H   W   P   F   Q   V   V   N   D   G   D   K
301/101                                          331/111
CCC AAG GTG CAG GTG AAC TAC AAG GGC GAG AGC CGG TCG TTC TTC CCG GAG GAG ATC TCG
P   K   V   Q   V   N   Y   K   G   E   S   R   S   F   F   P   E   E   I   S
361/121                                          391/131
TCC ATG GTG CTG ACG AAG ATG AAG GAG ATC GCT GAG GCG TAC CTG GGC CAC CCG GTG ACC
S   M   V   L   T   K   M   K   E   I   A   E   A   Y   L   G   H   P   V   T
421/141                                          451/151
AAC GCG GTG ATC ACG GTG CCC GCC TAC TTC AAC GAC TCT CAG CGG CAG GCC ACC AAG GAC
N   A   V   I   T   V   P   A   Y   F   N   D   S   Q   R   Q   A   T   K   D
481/161                                          511/171
GCG GGC GTG ATC GCC GGT CTA AAC GTG CTG CGG ATC ATC AAC GAG CCC ACG GCG GCC GCC
A   G   V   I   A   G   L   N   V   L   R   I   I   N   E   P   T   A   A   A
541/181                                          571/191
ATC GCC TAC GGG CTG GAC CGG ACC GGC AAG GGC GAG CGC AAC GTG CTC ATC TTC GAC CTG
I   A   Y   G   L   D   R   T   G   K   G   E   R   N   V   L   I   F   D   L
601/201                                          631/211
GGG GGC GGC ACG TTC GAC GTG TCC ATC CTG ACG ATC GAC GAC GGC ATC TTC GAG GTG AAG
G   G   G   T   F   D   V   S   I   L   T   I   D   D   G   I   F   E   V   K
661/221                                          691/231
GCC ACG GCG GGC GAC ACG CAC CTG GGA GGG GAG GAC TTC GAC AAC CGG CTG GTG AGC CAC
A   T   A   G   D   T   H   L   G   G   E   D   F   D   N   R   L   V   S   H
721/241                                          751/251
TTC GTG GAG GAG TTC AAG AGG AAG CAC AAG AAG GAC ATC AGC CAG AAC AAG CGC GCG GTG
F   V   E   E   F   K   R   K   H   K   K   D   I   S   Q   N   K   R   A   V
781/261                                          811/271
CGG CGG CTG CGC ACG GCC TGT GAG AGG GCC AAG AGG ACG CTG TCG TCC AGC ACC CAG GCC
R   R   L   R   T   A   C   E   R   A   K   R   T   L   S   S   S   T   Q   A
841/281                                          871/291
AGC CTG GAG ATC GAC TCT CTG TTC GAG GGC ATC GAC TTC TAC ACA TCC ATC ACG CGG GCG
S   L   E   I   D   S   L   F   E   G   I   D   F   Y   T   S   I   T   R   A
901/301                                          931/311
CGG TTC GAA GAG CTG TGC TCG GAC CTG TTC CGC GGC ACG CTG GAG CCC GTG GAG AAG GCC
R   F   E   E   L   C   S   D   L   F   R   G   T   L   E   P   V   E   K   A
961/321                                          991/331
CTG CGC GAC GCC AAG ATG GAC AAG GCC CAG ATC CAC GAC CTG GTG CTG GTG GGC GGC TCG
L   R   D   A   K   M   D   K   A   Q   I   H   D   L   V   L   V   G   G   S
1021/341                                         1051/351
ACG CGC ATC CCC AAG GTG CAG AAG CTG CTG CAG GAC TTC TTC AAC GGG CGC GAC CTG AAC
T   R   I   P   K   V   Q   K   L   L   Q   D   F   F   N   G   R   D   L   N
1081/361                                         1111/371
AAG AGC ATC AAC CCG GAC GAG GCG GTG GCC TAC GGG GCG GCG GTG CAG GCG GCC ATC CTG
K   S   I   N   P   D   E   A   V   A   Y   G   A   A   V   Q   A   A   I   L
1141/381                                         1171/391
ATG GGG GAC AAG TCG GAG AAC GTG CAG GAC CTG CTG CTG CTG GAC GTG GCG CCG CTG TCG
M   G   D   K   S   E   N   V   Q   D   L   L   L   L   D   V   A   P   L   S
1201/401                                         1231/411
CTG GGC CTG GAG ACT GCG GGC GGC GTG ATG ACG GCG CTC ATC AAG CGC AAC TCC ACC ATC
L   G   L   E   T   A   G   G   V   M   T   A   L   I   K   R   N   S   T   I
1261/421                                         1291/431
CCC ACC AAG CAG ACG CAG ACC TTC ACC ACC TAC TCG GAC AAC CAG CCC GGG GTG CTG ATC
P   T   K   Q   T   Q   T   F   T   T   Y   S   D   N   Q   P   G   V   L   I
```

Figure 13A

```
murine hsp70.1 -> Translate • 1-frame

1321/441                                1351/451
CAG GTG TAC GAG GGC GAG AGG GCC ATG ACG CGC GAC AAC AAC CTG CTG GGG CGC TTC GAG
Q   V   Y   E   G   E   R   A   M   T   R   D   N   N   L   L   G   R   F   E
1381/461                                1411/471
CTG AGC GGC ATC CCG CCG GCG CCC AGG GGC GTC CCG CAG ATC GAG GTG ACC TTC GAC ATC
L   S   G   I   P   P   A   P   R   G   V   P   Q   I   E   V   T   F   D   I
1441/481                                1471/491
GAC GCC AAC GGC ATC CTG AAC GTC ACG GCC ACC GAC AAG AGC ACC GGC AAG GCC AAC AAG
D   A   N   G   I   L   N   V   T   A   T   D   K   S   T   G   K   A   N   K
1501/501                                1531/511
ATC ACC ATC ACC AAC GAC AAG GGC CGC CTG AGC AAG GAG GAG ATC GAG CGC ATG GTG CAG
I   T   I   T   N   D   K   G   R   L   S   K   E   E   I   E   R   M   V   Q
1561/521                                1591/531
GAG GCC GAG CGC TAC AAG GCC GAG GAC GAG GTG CAG CGC GAC AGG GTG GCC GCC AAG AAC
E   A   E   R   Y   K   A   E   D   E   V   Q   R   D   R   V   A   A   K   N
1621/541                                1651/551
GCG CTC GAG TCC TAT GCC TTC AAC ATG AAG AGC GCC GTG GAG GAC GAG GGT CTC AAG GGC
A   L   E   S   Y   A   F   N   M   K   S   A   V   E   D   E   G   L   K   G
1681/561                                1711/571
AAG CTC AGC GAG GCT GAC AAG AAG AAG GTC CTG GAC AAG TGC CAG GAG GTC ATC TCC TGG
K   L   S   E   A   D   K   K   K   V   L   D   K   C   Q   E   V   I   S   W
1741/581                                1771/591
CTG GAC TCC AAC ACG CTG GCC GAC AAG GAG GAG TTC GTG CAC AAG CGG GAG GAG CTG GAG
L   D   S   N   T   L   A   D   K   E   E   F   V   H   K   R   E   E   L   E
1801/601                                1831/611
CGG GTG TGC AGC CCC ATC ATC AGT GGG CTG TAC CAG GGT GCG GGT GCT CCT GGG GCT GGG
R   V   C   S   P   I   I   S   G   L   Y   Q   G   A   G   A   P   G   A   G
1861/621                                1891/631
GGC TTC GGG GCC CAG GCG CCG CCG AAA GGA GCC TCT GGC TCA GGA CCC ACC ATC GAG GAG
G   F   G   A   Q   A   P   P   K   G   A   S   G   S   G   P   T   I   E   E
1921/641
GTG GAT TAG
V   D   *
```

Figure 13B

```
murine hsp70.1 -> Translate • 1-frame

DNA   sequence       1929  bp   ATGGCCAAGAAC ... GAGGTGGATTAG   linear
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                                                         571/191
                                                         AAG GGC GAG CGC AAC GTG CTC ATC TTC GAC CTG
                                                         K   G   E   R   N   V   L   I   F   D   L
601/201                                                  631/211
GGG GGC GGC ACG TTC GAC GTG TCC ATC CTG ACG ATC GAC GAC GGC ATC TTC GAG GTG AAG
G   G   G   T   F   D   V   S   I   L   T   I   D   D   G   I   F   E   V   K
661/221                                 691/231
GCC ACG GCG GGC GAC ACG CAC CTG GGA GGG GAG GAC TTC GAC AAC CGG CTG GTG AGC CAC
A   T   A   G   D   T   H   L   G   G   E   D   F   D   N   R   L   V   S   H
721/241                                 751/251
TTC GTG GAG GAG TTC AAG AGG AAG CAC AAG AAG GAC ATC AGC CAG AAC AAG CGC GCG GTG
F   V   E   E   F   K   R   K   H   K   K   D   I   S   Q   N   K   R   A   V
781/261                                 811/271
CGG CGG CTG CGC ACG GCG TGT GAG AGG GCC AAG AGG ACG CTG TCG TCC AGC ACC CAG GCC
R   R   L   R   T   A   C   E   R   A   K   R   T   L   S   S   S   T   Q   A
841/281                                 871/291
AGC CTG GAG ATC GAC TCT CTG TTC GAG GGC ATC GAC TTC TAC ACA TCC ATC ACG CGG GCG
S   L   E   I   D   S   L   F   E   G   I   D   F   Y   T   S   I   T   R   A
901/301                                 931/311
CGG TTC GAA GAG CTG TGC TCG GAC CTG TTC CGC GGC ACG CTG GAG CCC GTG GAG AAG GCC
R   F   E   E   L   C   S   D   L   F   R   G   T   L   E   P   V   E   K   A
961/321                                 991/331
CTG CGC GAC GCC AAG ATG GAC AAG GCC CAG ATC CAC GAC CTG GTG CTG GTG GGC GGC TCG
L   R   D   A   K   M   D   K   A   Q   I   H   D   L   V   L   V   G   G   S
1021/341                                1051/351
ACG CGC ATC CCC AAG GTG CAG AAG CTG CTG CAG GAC TTC TTC AAC GGG CGC GAC CTG AAC
T   R   I   P   K   V   Q   K   L   L   Q   D   F   F   N   G   R   D   L   N
1081/361                                1111/371
AAG AGC ATC AAC CCG GAC GAG GCG GTG GCC TAC GGG GCG GCG GTG CAG GCG GCC ATC CTG
K   S   I   N   P   D   E   A   V   A   Y   G   A   A   V   Q   A   A   I   L
1141/381                                1171/391
ATG GGG GAC AAG TCG GAG AAC GTG CAG GAC CTG CTG CTG CTG GAC GTG GCG CCC
M   G   D   K   S   E   N   V   Q   D   L   L   L   L   D   V   A   P
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Figure 14